

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/366,133DATE: 09/03/1999
TIME: 10:21:50

INPUT SET: S33187.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Pelleymounter, Mary Ann
Hecht, Randy I
Mann, Michael B

ENTERED

(ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 Dehavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 91230-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/366,133
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/920,608
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pessin, Karol M.
(C) REFERENCE/DOCKET NUMBER: A-345

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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47 (D) TOPOLOGY: linear

48

49 (ii) MOLECULE TYPE: cDNA

50

51

52

53

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55

56 TCTAGATTTG AGTTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAAGT 60

57

58 TCAGGACGAC ACCAAAACCT TAATTAAAAC GATCGTTACG CGTATCAACG ACATCAGTCA 120

59

60 CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA 180

61

62 CCCGATCCTA AGCTTGTTCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC 240

63

64 CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT 300

65

66 GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA 360

67

68 ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT 420

69

70 GTCCCGTCTG CAGGGTTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG 480

71

72 TTAATGGATC C 491

73

74 (2) INFORMATION FOR SEQ ID NO:2:

75

76 (i) SEQUENCE CHARACTERISTICS:

77 (A) LENGTH: 491 base pairs

78 (B) TYPE: nucleic acid

79 (C) STRANDEDNESS: double

80 (D) TOPOLOGY: linear

81

82 (ii) MOLECULE TYPE: cDNA

83

84

85

86

87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

88

89 AGATCTAAAC TCAAAATTGA AAATCTTCCT CTTATTGTA TACCATGGCT AGGTCTTTCA 60

90

91 AGTCCTGCTG TGGTTTTGGA ATTAATTTTG CTAGCAATGC GCATAGTTGC TGTAGTCAGT 120

92

93 GTGGGTCAGC CAGAGGCGAT TTGTGCGACA ATGGCCAGAC CTGAAGTAGG GCCCAGACGT 180

94

95 GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG 240

96

97 GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA 300

98

99 CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT 360

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100
101 TGGCCTTAGG GACCTGCCCC AGGACCTTCG TAGGGACATG TCGTGGCTTC AACCAACGAGA 420
102
103 CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAAA GAGGCCTTAC 480
104
105 AATTACCTAG G 491
106

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
1 5 10 15
Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
20 25 30
Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
35 40 45
Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
50 55 60
Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp
65 70 75 80
Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser
85 90 95
Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
100 105 110
Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
115 120 125
Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser
130 135 140
Pro Glu Cys
145

(2) INFORMATION FOR SEQ ID NO:4:

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153
154 (i) SEQUENCE CHARACTERISTICS:
155 (A) LENGTH: 454 base pairs
156 (B) TYPE: nucleic acid
157 (C) STRANDEDNESS: double
158 (D) TOPOLOGY: linear
159
160 (ii) MOLECULE TYPE: cDNA
161
162
163
164
165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
166
167 CATATGGTAC CGATCCAGAA AGTTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT 60
168
169 ACGCGTATCA ACGACATCAG TCACACCCAG TCGGTGAGCT CTAAACAGCG TGTTACAGGC 120
170
171 CTGGACTTCA TCCCGGGTCT GCACCCGATC CTGACCTTGT CCAAAATGGA CCAGACCCTG 180
172
173 GCTGTATACC AGCAGATCTT AACCTCCATG CCGTCCCGTA ACGTTCTTCA GATCTCTAAC 240
174
175 GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAAATC CTGCCACCTG 300
176
177 CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGGCG GGGTCCTGGA AGCATCCGGT 360
178
179 TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTGG 420
180
181 CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC 454
182
183 (2) INFORMATION FOR SEQ ID NO:5:
184
185 (i) SEQUENCE CHARACTERISTICS:
186 (A) LENGTH: 454 base pairs
187 (B) TYPE: nucleic acid
188 (C) STRANDEDNESS: double
189 (D) TOPOLOGY: linear
190
191 (ii) MOLECULE TYPE: cDNA
192
193
194
195
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
197
198 GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA 60
199
200 TGCGCATAGT TGCTGTAGTC AGTGTGGGTC AGCCACTCGA GATTGTGCGC ACAATGTCCG 120
201
202 GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC 180
203
204 CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG 240
205

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206 CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC 300
207
208 GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA 360
209
210 ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGAAGTCCT GTACGAAACC 420
211
212 GTCGACCTGG ACAGAGGCCC AACAATTACC TAGG 454
213

214 (2) INFORMATION FOR SEQ ID NO:6:

215
216 (i) SEQUENCE CHARACTERISTICS:

217 (A) LENGTH: 147 amino acids

218 (B) TYPE: amino acid

219 (C) STRANDEDNESS: single

220 (D) TOPOLOGY: linear
221

222 (ii) MOLECULE TYPE: protein
223
224
225
226

227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

228
229 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
230 1 5 10 15
231
232 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
233 20 25 30
234
235 Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
236 35 40 45
237
238 Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
239 50 55 60
240
241 Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
242 65 70 75 80
243
244 Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
245 85 90 95
246
247 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
248 100 105 110
249
250 Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
251 115 120 125
252
253 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
254 130 135 140
255
256 Pro Gly Cys
257 145
258

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SEQUENCE VERIFICATION REPORT
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Error

Original Text

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SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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Original Text

Corrected Text